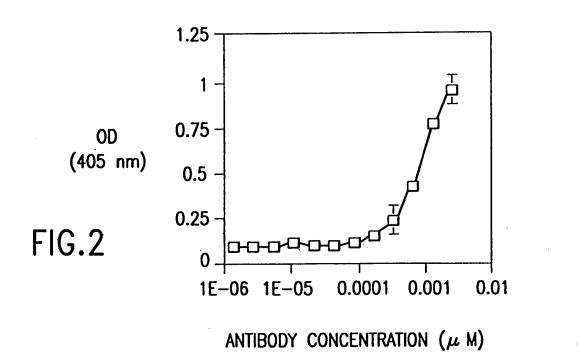
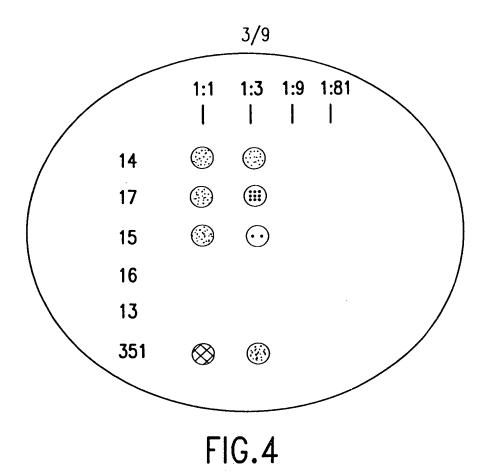
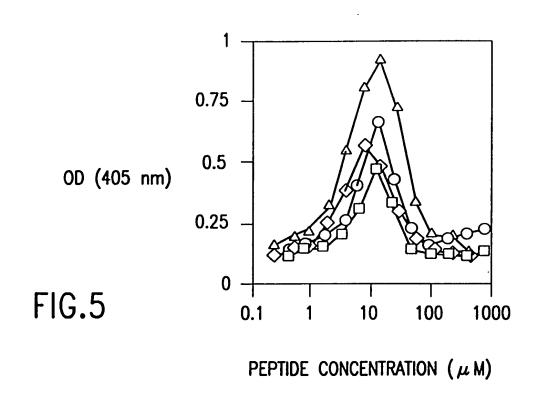


FIG.1



CLONE 14	GIINANDPLPFWFMSPYTPGPAPIDINASRALVS-NESG WQGTHFPYT LVSKNDSG CDR3L CDR2L (5/9 = 55.5 %) (7/8 = 87.5 %)
CLONE 17	DL-SRNLDFGRFLLYNAYVPGFTPTFISLTAEHLSSPKG LVSKN-DSG WQGTHF-P-YT CDR2L CDR3L (6/8 = 75 %) (6/9 = 66.6 %)
CLONE 15	CGRAYCL-SGNYNIFGALFPGVSTPYADVGHDDAQSWRR LVSKN-DS-G WQG-THFPYT CDR2L CDR3L (4/8 = 50 %) (6/9 = 66.6 %)
CLONE 13	RCSPIW-GIS-YPFGLLSSNPGVCHSSDAET-NIRNDILTT WQG-THFPYT GSDN-K-SVL CDR3L CDR2L(REV) (6/9 = 66.6 %) (4/8 = 50 %)
CLONE 16	GHSNYCFVSTLGMPIVGFP-SINARGLIHYGGSDPRLAA WQGTHFPYT GSDNKSVL CDR3L CDR2L(REV) (3/9 = 33.3 %) (5/8 = 62.5 %)





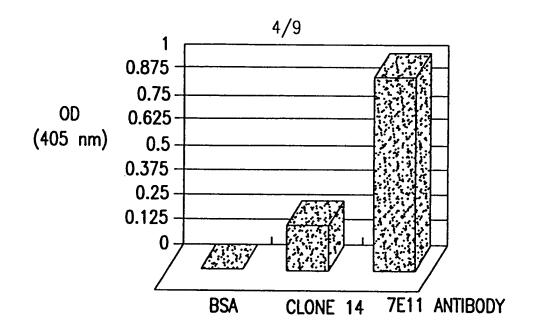


FIG.6

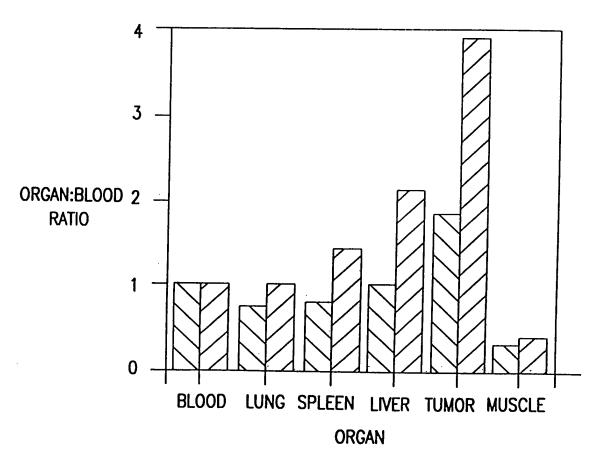
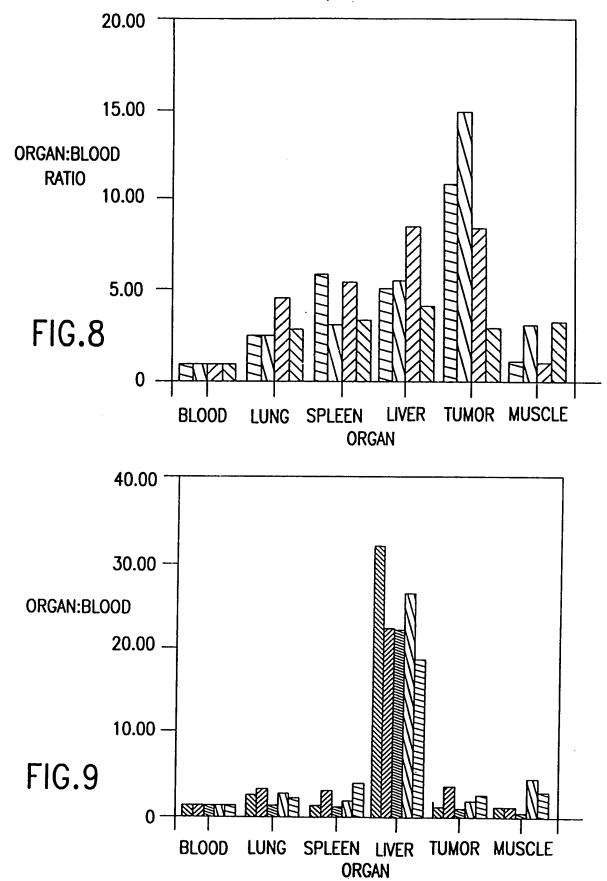


FIG.7





```
Sac II
c.tgt.gcc.tcg.agB.(NNB)<sub>12</sub>.Ncc.gcg.g
                                   gg.cgc.cNV.(NNV)<sub>12</sub>.aga.tct.cgt.gtc
        N=A,G,T,C
        B=G,T,C
                                           FILL IN WITH DNA POLYMERASE
        V=G,A,C
              Xho I
                                       Ala
c.tgt.gcc.tcg.agB.(NNB)<sub>12</sub>.Ncc.gcg.g
                                   gg.cgc.cNV.(NNV)<sub>12</sub>.aga.tct.cgt.gtc
                                                             Xba I
                                          CLEAVE WITH Xho I + Xba I
             tcg.agB.(NNB)<sub>12</sub>.Ncc.gcg.g
                                   gg.cgc.cNV.(NNV)<sub>12</sub>.tga.tc
                                          LIGATE WITH Xho I + Xba I-
CLEAVED M13 m663 VECTOR
                                          ELECTROPORATE INTO XL1-BLUE
```

LIBRARY OF PIII-RANDOM SEQUENCE FUSION PROTEINS

. . . S H S S (S/R)
$$X_{12}\pi A \partial X_{12}$$
 S R P S R T . . . π = S,P,T Π R A θ = V,A,D,E, Π R G SIGNAL PEPTIDASE CLEAVAGE SITE

G TGT GTC TCG AGN (NNB)20NAC GCC AN

N=A,C,G,T B=C,G,T V=A,C,G NTG CGG TNV (NNV)₁₅ AGA TCT GTG TTG

FILL IN WITH SEQUENASE

Xho I

G TGT GTC TCG AGN (NNB)20NAC GCC AN

NTG CGG TNV (NNV)₁₅ AGA TCT GTG TTG Xba I

TOTAL VIEW T AND VIEW

TCG AGN (NNB)20 NAC GCC AN

NTG CGG TNV (NNV)₁₅ AGA TC

LIGATE WITH Xho I + Xba I-CLEAVED M13mp18Xa

ELECTROTRANSFORM E. coli JS5

D38 GENETIC DIVERSITY LIBRARY DISPLAYED AS RANDOM N-TERMINAL PILI FUSIONS

. . H S S (S/R) X_{20} (Y/H/N/D) A (I/M/T/N/K/S/R) X_{15} S R SIGNAL PEPTIDASE CLEAVAGE SITE

FIG. 11

G TGT GTC TCG AGN (NNB)20GGT TGT GGT

N=A,C,G,T CCA ACA CCA (NNV)₂₀ AGA TCT GTG TTG

B=C,G,T V=A,C,G

FILL IN WITH SEQUENASE

Xho I

G TGT GTC TCG AGN (NNB)20GGT TGT GGT

CCA ACA CCA (NNV) AGA TCT GTG TTG Xba I

RESTRICT WITH Xho I AND Xba I

TCG AGN (NNB)20 GGT TGT GGT

CCA ACA CCA (NNV)20 AGA TC

| LIGATE WITH Xho I + Xba I-| CLEAVED M13mp18Xa

ELECTROTRANSFORM E. coli JS5

DC43 GENETIC DIVERSITY LIBRARY DISPLAYED AS RANDOM N-TERMINAL PIII FUSIONS

. . H S₁S (S/R) X₂₀G C G X₂₀S R

SIGNAL PEPTIDASE CLEAVAGE SITE

GAPVWRGNPRWRGPCS-CCS-ggs-ggs-tts-aas-tgs-ccs-GG-IGC-GGNGPMCNTFTPARGGSRNNGP 5′ 995-9c5-ccs-gts-tgs-ags-ggs-aas-ccs-ggs-ggs-tts-aas-tgs-ccs-GG-IGC-GGG3′ PP-I oligo I

MP-1 oligo 2

FIG.13